

SEQUENCE LISTING

<110> Glotzer, Michael
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Kaitna, Susanne

<120> Cyk-4 polypeptides, DNA molecules encoding them and their use in
screening methods

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<151> 2000-06-19

<150> BP 01 110 554.1

<151> 2001-04-30

<150> 60/241,231

<151> 2000-10-18

<150> To be determined

<151> 2001-06-13

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<170> PatentIn Ver. 2.1

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Gln Leu Val Arg Arg Val Glu Ile Leu Ser Glu Gly Asn Glu Val Gln
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Phe Ile Gln Leu Ala Lys Asp Phe Glu Asp Phe Arg Lys Lys Trp Gln
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Arg Thr Asp His Glu Leu Gly Lys Tyr Lys Asp Leu Leu Met Lys Ala
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Tyr Gln Arg Thr Asn Gln Glu Leu Glu Lys Phe Lys Asp Leu Leu Leu
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ttt ttc cct gct cag tac ctc aag taa agctgtgtct gcctgtgttt	2041
Phe Phe Pro Ala Pro Tyr Leu Lys	
625	

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gagccctcag cgggatgggc cgggccactg atctgaggat gcttcaattc tgtctgggtt 2521

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gcctggattt tgcagtcata gtcagggtga tctgaagcgg aattcgttct gatgcctgac 2641

ccccttggtt gtccagtggg gcccatctaa aaagtcagct agcagttcag aagacaattt 2701

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tatatatgtg aacattggct tttttggtta gcattttcca gtgttcaaaa tggcttcctt 2821

ccttgggatg ttttctgacc catactaacc cttacctgta acatgtatct ggaatattat 2881

gtggaaaaaa taaatagctt tttcaaagtg aactttcc 2919

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<212> PRT

<213> Mus musculus

<400> 4

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20 25 30

Gln Val Val Lys Asp Phe Glu Asp Phe Arg Lys Lys Tyr Gln Arg Thr
35 40 45

Asn Gln Glu Leu Glu Lys Phe Lys Asp Leu Leu Leu Lys Ala Glu Thr
50 55 60

Gly Arg Ser Ala Leu Asp Val Lys Leu Lys His Ala Arg Asn Gln Val
65 70 75 80

Asp Val Glu Ile Lys Arg Arg Gln Arg Ala Glu Ala Glu Cys Ala Lys
85 90 95

Leu Glu Gln Gln Ile Gln Leu Ile Arg Asp Ile Leu Met Cys Asp Thr
100 105 110

Ser Gly Ser Ile Gln Leu Ser Glu Glu Gln Lys Ser Ala Leu Ala Phe
115 120 125

Leu Asn Arg Gly Gln Ala Ser Ser Gly His Ala Gly Asn Asn Arg Leu
130 135 140

Ser Thr Ile Asp Glu Ser Gly Ser Ile Leu Ser Asp Ile Ser Phe Asp
145 150 155 160

Lys Thr Asp Glu Ser Leu Asp Trp Asp Ser Ser Leu Val Lys Asn Phe
165 170 175

Lys Met Lys Lys Arg Glu Lys Arg Arg Ser Asn Ser Arg Gln Phe Ile
180 185 190

Asp Gly Pro Pro Gly Pro Val Lys Lys Thr Cys Ser Ile Gly Ser Thr
195 200 205

Val Asp Gln Ala Asn Glu Ser Ile Val Ala Lys Thr Thr Val Thr Val
210 215 220

Pro Ser Asp Gly Gly Pro Ile Glu Ala Val Ser Thr Ile Glu Thr Leu
225 230 235 240

Pro Ser Trp Thr Arg Ser Arg Gly Lys Ser Gly Pro Leu Gln Pro Val
245 250 255

Asn Ser Asp Ser Ala Leu Asn Ser Arg Pro Leu Glu Pro Arg Thr Asp
260 265 270

Thr Asp Asn Leu Gly Thr Pro Gln Asn Thr Gly Gly Met Arg Leu His
275 280 285

Asp Phe Val Ser Lys Thr Val Ile Lys Pro Glu Ser Cys Val Pro Cys
290 295 300

Gly Lys Arg Ile Lys Phe Gly Lys Leu Ser Leu Lys Cys Arg Asp Cys
305 310 315 320

Arg Leu Val Ser His Pro Glu Cys Arg Asp Arg Cys Pro Leu Pro Cys
325 330 335

Ile Pro Pro Leu Val Gly Thr Pro Val Lys Ile Gly Glu Gly Met Leu
340 345 350

Ala Asp Phe Val Ser Gln Ala Ser Pro Met Ile Pro Ala Ile Val Val
355 360 365

Ser Cys Val Asn Glu Ile Glu Gln Arg Gly Leu Thr Glu Ala Gly Leu
370 375 380

Tyr Arg Ile Ser Gly Cys Asp Arg Thr Val Lys Glu Leu Lys Glu Lys
385 390 395 400

Phe Leu Lys Val Lys Thr Val Pro Leu Leu Ser Lys Val Asp Asp Ile
405 410 415

His Val Ile Cys Ser Leu Leu Lys Asp Phe Leu Arg Asn Leu Lys Glu
420 425 430

Pro Leu Leu Thr Phe Trp Leu Ser Lys Ala Phe Met Glu Ala Ala Glu
435 440 445

Ile Thr Asp Glu Asp Asn Ser Thr Ala Ala Met Tyr Gln Ala Val Ser
450 455 460

Glu Leu Pro Gln Ala Asn Arg Asp Thr Leu Ala Phe Leu Met Ile His
465 470 475 480

Leu Gln Arg Val Ser Gln Ser Pro Asp Thr Lys Met Asp Ile Ala Asn
485 490 495

Leu Ala Lys Val Phe Gly Pro Thr Ile Val Ala His Thr Val Pro Asn
500 505 510

Pro Asp Pro Val Thr Met Phe Gln Asp Ile Lys Arg Gln Leu Lys Val
515 520 525

Val Glu Arg Leu Leu Ser Leu Pro Leu Glu Tyr Trp Asn Gln Phe Met
530 535 540

Met Val Asp Gln Glu Asn Ile Asp Ser Gln Arg Gly Asn Gly Asn Ser
545 550 555 560

Thr Pro Arg Thr Pro Asp Val Lys Val Ser Leu Leu Gly Pro Val Thr
565 570 575

Thr Pro Glu Phe Gln Leu Val Lys Thr Pro Leu Ser Ser Ser Leu Ser
580 585 590

Gln Arg Leu Tyr Asn Leu Ser Lys Ser Thr Pro Arg Phe Gly Asn Lys

605

atg	aag	tcc	agt	aca	tca	aaa	gag	aag	gtg	tgc	ggc	gaa	aac	tcg	cgt	48
Met	Lys	Ser	Ser	Thr	Ser	Lys	Glu	Lys	Val	Cys	Gly	Glu	Asn	Ser	Arg	
1				5					10					15		
cac	att	ttc	aac	atg	att	cta	aac	tca	cag	cga	ccg	caa	ttc	gat	att	96
His	Ile	Phe	Asn	Met	Ile	Leu	Asn	Ser	Gln	Arg	Pro	Gln	Phe	Asp	Ile	
			20					25					30			
aag	gat	ata	gga	atg	ttt	cat	ttg	att	gat	gag	att	gag	cgt	ctc	cgc	144
Lys	Asp	Ile	Gly	Met	Phe	His	Leu	Ile	Asp	Glu	Ile	Glu	Arg	Leu	Arg	
		35					40					45				
aag	ctg	tgg	aaa	gat	tcc	gag	gaa	tcc	aaa	aag	cgg	ctg	aat	gca	gat	192
Lys	Leu	Trp	Lys	Asp	Ser	Glu	Glu	Ser	Lys	Lys	Arg	Leu	Asn	Ala	Asp	
	50					55					60					
atg	aga	gag	gcc	gaa	gaa	gca	ctt	gca	aaa	gct	cgc	aag	aag	ctg	gca	240
Met	Arg	Glu	Ala	Glu	Glu	Ala	Leu	Ala	Lys	Ala	Arg	Lys	Lys	Leu	Ala	
65				70					75					80		
atg	ttc	gat	atc	gat	gtc	aaa	gac	act	cag	aaa	cat	tta	cgc	gcg	ttg	288
Met	Phe	Asp	Ile	Asp	Val	Lys	Asp	Thr	Gln	Lys	His	Leu	Arg	Ala	Leu	
				85					90					95		
atg	gaa	gaa	aat	aag	gcg	ttg	aag	ctc	gat	cta	aac	gtc	tac	gag	act	336
Met	Glu	Glu	Asn	Lys	Ala	Leu	Lys	Leu	Asp	Leu	Asn	Val	Tyr	Glu	Thr	
			100					105				110				

cgt gaa aag cag ctg aaa gat gcg atg aag aac ggt ata ttc aat agt	384
Arg Glu Lys Gln Leu Lys Asp Ala Met Lys Asn Gly Ile Phe Asn Ser	
115 120 125	
ctc acc aag gaa gac cgc gat cag ttc aag ttt ctt cac gag cca ctg	432
Leu Thr Lys Glu Asp Arg Asp Gln Phe Lys Phe Leu His Glu Pro Leu	
130 135 140	
gtc cgg aca tac tcg aaa cgg gtg cag cag agg cat cca cat ttg atg	480
Val Arg Thr Tyr Ser Lys Arg Val Gln Gln Arg His Pro His Leu Met	
145 150 155 160	
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Glu Asp Thr Gln Asp Asp Glu Asp Asp Ser Glu Val Asp Tyr Asp Glu	
165 170 175	
act gga gac agt ttc gag gaa gtt att cat ttg cgc aat gga aga gag	576
Thr Gly Asp Ser Phe Glu Glu Val Ile His Leu Arg Asn Gly Arg Glu	
180 185 190	
gtc aga aga agc tca gct gct gga aac gca gtt ggt ggc aag cgg aga	624
Val Arg Arg Ser Ser Ala Ala Gly Asn Ala Val Gly Gly Lys Arg Arg	
195 200 205	
agc gcg tca gca cat gcg att act gct gct gcc aat tcg aag agg agc	672
Ser Ala Ser Ala His Ala Ile Thr Ala Ala Ala Asn Ser Lys Arg Ser	
210 215 220	
aga agc cgt gtt atg aca gct act ata gat gaa gag ccg aat gag ggt	720
Arg Ser Arg Val Met Thr Ala Thr Ile Asp Glu Glu Pro Asn Glu Gly	
225 230 235 240	
ggt aca cct cca aaa aga tgc cgt gat gat ggt tct aca cct cat caa	768
Gly Thr Pro Pro Lys Arg Cys Arg Asp Asp Gly Ser Thr Pro His Gln	
245 250 255	
gaa atg aca act acc acc act acc acc acc act act att cat aac	816
Glu Met Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr	
260 265 270	
tct cga gct cag aac cag gac ccg cca cgt gtc tca ctt cac cgc cag	864
Ser Arg Ala Gln Asn Gln Asp Pro Pro Arg Val Ser Leu His Arg Gln	
275 280 285	

ctc acc cgc agg agc ttg agc tgt gga agt att cca tca tgc gat caa	912
Leu Thr Arg Arg Ser Leu Ser Cys Gly Ser Ile Pro Ser Cys Asp Gln	
290 295 300	
aca cca gga caa acc aca aat aac atc ggc ctc ggc atg tgc tcc gcc	960
Thr Pro Gly Gln Thr Thr Asn Asn Ile Gly Leu Gly Met Ser Ser Ala	
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att ctc acc aaa agc aca ctt gat atc cga acc ctg aaa cgt ggc acg	1008
Ile Leu Thr Lys Ser Thr Leu Asp Ile Arg Thr Leu Lys Arg Gly Thr	
325 330 335	
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Pro Ala Trp Thr Asn Gly Thr Thr Arg Asp Ile Ala Met Arg Pro His	
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acg ttt ata gag gca gga atc aaa gcg atg cga aaa tgc gac aaa tgt	1104
Thr Phe Ile Glu Ala Gly Ile Lys Ala Met Arg Lys Cys Asp Lys Cys	
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Ala Thr Ala Leu Lys Leu Ala Thr Ser Met Lys Cys Arg Asp Cys His	
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Gln Val Val His Arg Ser Cys Cys Asn Lys Leu His Leu Pro Cys Ile	
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cca cgc ccc aag acg atg atg acg ccg aaa tcc gca tta cgt gga gcc	1248
Pro Arg Pro Lys Thr Met Met Thr Pro Lys Ser Ala Leu Arg Gly Ala	
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Lys Pro Gly Ala Gly Glu Phe Arg Leu Gln Asp Leu Cys Thr Ser Ala	
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Lys Pro Met Ile Pro Ala Ala Val Ile His Cys Val Val Ala Leu Glu	
435 440 445	
gct cgt gga ctc acg cag gaa ggt att tac cgc gtt cct ggg cag gtt	1392
Ala Arg Gly Leu Thr Gln Gly Ile Tyr Arg Val Pro Gly Gln Val	
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Arg Thr Val Asn Val Leu Leu Asp Glu Leu Arg Ser Lys Thr Val Pro	
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Asn Val Gly Leu His Asp Val Glu Val Ile Thr Asp Thr Leu Lys Arg	
485 490 495	
ttc cta aga gat ctt aaa gac ccg ttg atc cca aga acg tct cgt caa	1536
Phe Leu Arg Asp Leu Lys Asp Pro Leu Ile Pro Arg Thr Ser Arg Gln	
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gag ctc atc gtt gct gca aac ctc tac tct acg gat cca gat aat gga	1584
Glu Leu Ile Val Ala Ala Asn Leu Tyr Ser Thr Asp Pro Asp Asn Gly	
515 520 525	
cgt ctc gcc ctg aat cga gtg atc tgt gag ctc ccc caa gcg aat cga	1632
Arg Leu Ala Leu Asn Arg Val Ile Cys Glu Leu Pro Gln Ala Asn Arg	
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gac acc ctc gcc tac ctt ttc att cac tgg cgc aaa gtt atc gca caa	1680
Asp Thr Leu Ala Tyr Leu Phe Ile His Trp Arg Lys Val Ile Ala Gln	
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Ser Ser Arg Asn Lys Met Asn Cys Glu Ala Met Ala Arg Met Val Ala	
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Pro Ala Val Met Gly His Pro Val Lys Gln Ser Gln Ser Gln Ala Ile	
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Ala Gly Arg Asp Ala Thr Asp Cys His Arg Ala Met Thr Ala Leu Phe	
595 600 605	
gaa ttt gat gat gta tat tgg caa cga ttc cta ggg aca tct gca gtt	1872
Glu Phe Asp Asp Val Tyr Trp Gln Arg Phe Leu Gly Thr Ser Ala Val	
610 615 620	
tcc atg gct tct aat caa att gaa acg gct cga cat cag gac aat ttt	1920
Ser Met Ala Ser Asn Gln Ile Glu Thr Ala Arg His Gln Asp Asn Phe	
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Thr Pro Leu Leu Ala Arg Ser Ala Asn Ala Thr Arg Ala Arg Gly Ala
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cat ctg ctg ggg tcg atg ttc cac gat tag 2046

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<211> 681

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<213> Caenorhabditis elegans

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Lys Asp Ile Gly Met Phe His Leu Ile Asp Glu Ile Glu Arg Leu Arg
35 40 45

Lys Leu Trp Lys Asp Ser Glu Glu Ser Lys Lys Arg Leu Asn Ala Asp
50 55 60

Met Arg Glu Ala Glu Glu Ala Leu Ala Lys Ala Arg Lys Lys Leu Ala
65 70 75 80

Met Phe Asp Ile Asp Val Lys Asp Thr Gln Lys His Leu Arg Ala Leu
85 90 95

Met Glu Glu Asn Lys Ala Leu Lys Leu Asp Leu Asn Val Tyr Glu Thr
100 105 110

Arg Glu Lys Gln Leu Lys Asp Ala Met Lys Asn Gly Ile Phe Asn Ser
115 120 125

Leu Thr Lys Glu Asp Arg Asp Gln Phe Lys Phe Leu His Glu Pro Leu
130 135 140

Val Arg Thr Tyr Ser Lys Arg Val Gln Gln Arg His Pro His Leu Met
145 150 155 160

Glu Asp Thr Gln Asp Asp Glu Asp Asp Ser Glu Val Asp Tyr Asp Glu
165 170 175

Thr Gly Asp Ser Phe Glu Glu Val Ile His Leu Arg Asn Gly Arg Glu
180 185 190

Val Arg Arg Ser Ser Ala Ala Gly Asn Ala Val Gly Gly Lys Arg Arg
195 200 205

Ser Ala Ser Ala His Ala Ile Thr Ala Ala Ala Asn Ser Lys Arg Ser
210 215 220

Arg Ser Arg Val Met Thr Ala Thr Ile Asp Glu Glu Pro Asn Glu Gly
225 230 235 240

Gly Thr Pro Pro Lys Arg Cys Arg Asp Asp Gly Ser Thr Pro His Gln
245 250 255

Glu Met Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Ile His Asn
260 265 270

Ser Arg Ala Gln Asn Gln Asp Pro Pro Arg Val Ser Leu His Arg Gln
275 280 285

Leu Thr Arg Arg Ser Leu Ser Cys Gly Ser Ile Pro Ser Cys Asp Gln
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Thr Pro Gly Gln Thr Thr Asn Asn Ile Gly Leu Gly Met Ser Ser Ala
305 310 315 320

Ile Leu Thr Lys Ser Thr Leu Asp Ile Arg Thr Leu Lys Arg Gly Thr
325 330 335

Pro Ala Trp Thr Asn Gly Thr Thr Arg Asp Ile Ala Met Arg Pro His
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Thr Phe Ile Glu Ala Gly Ile Lys Ala Met Arg Lys Cys Asp Lys Cys
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Ala Thr Ala Leu Lys Leu Ala Thr Ser Met Lys Cys Arg Asp Cys His
370 375 380

Gln Val Val His Arg Ser Cys Cys Asn Lys Leu His Leu Pro Cys Ile
385 390 395 400

Pro Arg Pro Lys Thr Met Met Thr Pro Lys Ser Ala Leu Arg Gly Ala
405 410 415

Lys Pro Gly Ala Gly Glu Phe Arg Leu Gln Asp Leu Cys Thr Ser Ala
420 425 430

Lys Pro Met Ile Pro Ala Ala Val Ile His Cys Val Val Ala Leu Glu
435 440 445

Ala Arg Gly Leu Thr Gln Glu Gly Ile Tyr Arg Val Pro Gly Gln Val
450 455 460

Arg Thr Val Asn Val Leu Leu Asp Glu Leu Arg Ser Lys Thr Val Pro

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Phe	Leu	Arg	Asp	Leu	Lys	Asp	Pro	Leu	Ile	Pro	Arg	Thr	Ser	Arg	Gln
515				520				525				530			
Glu	Leu	Ile	Val	Ala	Ala	Asn	Leu	Tyr	Ser	Thr	Asp	Pro	Asn	Asp	Gly
535				540				545				550			
Arg	Leu	Ala	Leu	Asn	Arg	Val	Ile	Cys	Glu	Leu	Pro	Gln	Ala	Asn	Arg
555				560				565				570			
Asp	Thr	Leu	Ala	Tyr	Leu	Phe	Ile	His	Trp	Arg	Lys	Val	Ile	Ala	Gln
575				580				585				590			
Ser	Ser	Arg	Asn	Lys	Met	Asn	Cys	Glu	Ala	Met	Ala	Arg	Met	Val	Ala
595				600				605				610			
Pro	Ala	Val	Met	Gly	His	Pro	Val	Lys	Gln	Ser	Gln	Ser	Gln	Ala	Ile
615				620				625				630			
Ala	Gly	Arg	Asp	Ala	Thr	Asp	Cys	His	Arg	Ala	Met	Thr	Ala	Leu	Phe
635				640				645				650			
Glu	Phe	Asp	Asp	Val	Tyr	Trp	Gln	Arg	Phe	Leu	Gly	Thr	Ser	Ala	Val
655				660				665				670			
Ser	Met	Ala	Ser	Asn	Gln	Ile	Glu	Thr	Ala	Arg	His	Gln	Asp	Asn	Phe
675				680				685				690			
Ala	Leu	Cys	Asp	Arg	Ser	Ile	Leu	Gly	Pro	Val	Thr	Thr	Ser	Pro	Ala
695				700				705				710			
Thr	Pro	Leu	Leu	Ala	Arg	Ser	Ala	Asn	Ala	Thr	Arg	Ala	Arg	Gly	Ala
715				720				725				730			
His	Leu	Leu	Gly	Ser	Met	Phe	His	Asp							